

WHAT IS CLAIMED IS:

1 1. An isolated polynucleotide molecule comprising
2 an operably linked transcriptional promoter, a polynucleotide
3 sequence encoding a PIV genome or antigenome, and a
4 transcriptional terminator, wherein said polynucleotide
5 sequence encoding said PIV genome or antigenome is modified by
6 introduction of a heterologous PIV sequence selected from a
7 HPIV1 sequence, a HPIV2 sequence, a HPIV3 sequence, a BPIV
8 sequence or a MPIV sequence to form a chimeric PIV genome or
9 antigenome.

1 2. The isolated polynucleotide molecule of claim
2 1, wherein a gene or gene segment of human PIV3 is replaced
3 with a counterpart gene or gene segment from a heterologous
4 PIV.

1 3. The isolated polynucleotide molecule of claim
2 2, wherein the counterpart gene or gene segment is a HN or F
3 glycoprotein gene or gene segment of HPIV1 or HPIV2.

1 4. The isolated polynucleotide molecule of claim
2 2, wherein an HN or F glycoprotein gene of PIV1 or PIV2 is
3 substituted for the counterpart HN or F glycoprotein gene of
4 HPIV3.

1 5. The isolated polynucleotide molecule of claim
2 1, wherein the polynucleotide sequence encoding the genome or
3 antigenome incorporates a BPIV gene or gene segment.

1 6. The isolated polynucleotide molecule of claim
2 1, which incorporates a heterologous sequence from RSV.

1 7. The isolated polynucleotide molecule of claim
2 6, wherein the heterologous sequence from RSV is a G or F gene
3 or gene segment.

1 8. The isolated polynucleotide molecule of claim
2 1, which incorporates a heterologous sequence from measles
3 virus.

1 9. The isolated polynucleotide molecule of claim
2 8, wherein the heterologous sequence from measles virus is a
3 HA or F gene or gene segment.

1 10. An isolated polynucleotide molecule comprising
2 an operably linked transcriptional promoter, a polynucleotide
3 sequence encoding a PIV genome or antigenome, and a
4 transcriptional terminator, wherein said polynucleotide
5 sequence encoding said PIV genome or antigenome is selected
6 from the group consisting of:
7 i) p218(131) (SEQ ID NO: 1);
8 ii) p3/7(131) (SEQ ID NO: 14);
9 iii) p3/7(131)2G (SEQ ID NO: 15); or
10 iv) the isolated polynucleotide of i), ii) or iii)
11 modified by introduction of a heterologous PIV sequence
12 selected from a HPIV1 sequence, a HPIV2 sequence, a BPIV
13 sequence or a MPIV sequence or by a nucleotide insertion,
14 rearrangement, deletion or substitution specifying a
15 phenotypic alteration selected from attenuation, temperature-
16 sensitivity, cold-adaptation, small plaque size, host range
17 restriction, or a change in an immunogenic epitope of PIV.

1 11. An isolated polynucleotide molecule comprising
2 an operably linked transcriptional promoter, a polynucleotide
3 sequence encoding a PIV genome or antigenome, and a
4 transcriptional terminator, wherein said polynucleotide
5 sequence encoding said PIV genome or antigenome is modified by
6 a nucleotide insertion, rearrangement, deletion or
7 substitution.

1 12. The isolated polynucleotide molecule of claim
2 11, wherein said nucleotide insertion, rearrangement, deletion
3 or substitution specifies a phenotypic alteration selected
4 from attenuation, temperature-sensitivity, cold-adaptation,

1 small plaque size, host range restriction, or a change in an
2 immunogenic epitope of PIV.

1 13. The isolated polynucleotide molecule of claim
2 12, wherein said polynucleotide sequence encoding said PIV
3 genome or antigenome incorporates multiple *ts* mutations.

1 14. The isolated polynucleotide molecule of claim
2 12, wherein said polynucleotide sequence encoding said PIV
3 genome or antigenome incorporates multiple non-*ts* attenuating
4 mutations.

1 15. The isolated polynucleotide molecule of claim
2 11, wherein said polynucleotide sequence encoding said PIV
3 genome or antigenome incorporates one or more mutations of JS
4 cp45.

1 16. The isolated polynucleotide molecule of claim
2 15, wherein said polynucleotide sequence encoding said PIV
3 genome or antigenome encodes at least one amino acid
4 substitution in the polymerase L protein.

1 17. The isolated polynucleotide molecule of claim
2 16, wherein the amino acid substitution in the polymerase L
3 protein occurs at a position corresponding to Tyr₉₄₂, Leu₉₉₂, or
4 Thr₁₅₅₈ of JS cp45.

1 18. The isolated polynucleotide molecule of claim
2 11, wherein said polynucleotide sequence encoding said PIV
3 genome or antigenome encodes at least one amino acid
4 substitution in the N protein.

1 19. The isolated polynucleotide molecule of claim
2 28, wherein the amino acid substitution in the N protein
3 occurs at a position corresponding to residues Val₉₆ or Ser₃₈₉
4 of JS cp45.

1 20. The isolated polynucleotide molecule of claim
2 11, wherein said polynucleotide sequence encoding said PIV
3 genome or antigenome encodes an amino acid substitution in the
4 C protein.

1 21. The isolated polynucleotide molecule of claim
2 20, wherein the amino acid substitution in the C protein
3 occurs at a position corresponding to Ile₉₆ of JS cp45.

1 22. The isolated polynucleotide molecule of claim
2 11, wherein said polynucleotide sequence encoding said PIV
3 genome or antigenome encodes at least one amino acid
4 substitution in the F protein.

1 23. The isolated polynucleotide molecule of claim
2 22, wherein the amino acid substitution in the F protein
3 occurs at a position corresponding to Ile₄₂₀ or Ala₄₅₀ of JS
4 cp45.

1 24. The isolated polynucleotide molecule of claim
2 11, wherein said polynucleotide sequence encoding said PIV
3 genome or antigenome encodes an amino acid substitution in the
4 HN protein.

1 25. The isolated polynucleotide molecule of claim
2 24, wherein the amino acid substitution in the HN protein
3 occurs at a position corresponding to residue Val₃₈₄ of JS
4 cp45.

1 26. The isolated polynucleotide molecule of claim
2 11, wherein said polynucleotide sequence encoding said PIV
3 genome or antigenome incorporates at least one mutation in a
4 3' leader sequence.

1 27. The isolated polynucleotide molecule of claim
2 26, wherein the mutation in the 3' leader occurs at a position
3 corresponding to nucleotide 23, 24, 28, or 45 of JS cp45.

1 28. The isolated polynucleotide molecule of claim
2 11, wherein said polynucleotide sequence encoding said PIV
3 genome or antigenome incorporates a mutation in a N gene start
4 sequence.

1 29. The isolated polynucleotide molecule of claim
2 28, wherein the mutation in the N gene start sequence occurs
3 at a position corresponding to nucleotide 62 of JS *cp45*.

1 30. The isolated polynucleotide molecule of claim
2 12, wherein said polynucleotide sequence encoding said PIV
3 genome or antigenome incorporates a plurality and up to a full
4 complement of mutations present in *rcp45*, *rcp45* 3'NCMFHN,
5 *rcp45* 3'NL, *rcp45* 3'N, or *rcp45* F.

1 31. The isolated polynucleotide molecule of claim
2 12, which is an antigenomic cDNA selected from *rcp45*, *rcp45*
3 3'NCMFHN, *rcp45* 3'NL, *rcp45* 3'N, *rcp45* L, *rcp45* F, *rcp45* M,
4 *rcp45* HN, or *rcp45* C.

1 32. The isolated polynucleotide molecule of claim
2 11, wherein said polynucleotide sequence encoding said PIV
3 genome or antigenome incorporates a mutation stabilized by
4 multiple nucleotide substitutions in a codon specifying the
5 mutation.

1 33. The isolated polynucleotide molecule of claim
2 11, wherein said polynucleotide sequence encoding said PIV
3 genome or antigenome incorporates a heterologous sequence from
4 HPIV1, HPIV2, HPIV3, BPIV or MPIV to form a chimeric genome or
5 antigenome.

1 34. The isolated polynucleotide molecule of claim
2 33, wherein said chimeric genome or antigenome incorporates
3 one or more *ts* mutations.

1 35. The isolated polynucleotide molecule of claim
2 33, wherein said chimeric genome or antigenome incorporates
3 one or more non-ts attenuating mutations.

1 36. The isolated polynucleotide molecule of claim
2 33, wherein said chimeric genome or antigenome incorporates
3 one or more mutations of JS cp45.

1 37. The isolated polynucleotide molecule of claim
2 36, wherein said one or more mutations of JS cp45 occur in one
3 or more PIV proteins selected from L, M, N, C, F, or HN or in
4 a PIV extragenic sequence selected from a 3' leader or N-gene
5 start sequence.

1 38. The isolated polynucleotide molecule of claim
2 33, wherein said chimeric genome or antigenome incorporates
3 multiple mutations each specifying a phenotype selected from
4 attenuation, temperature-sensitivity, cold-adaptation, small
5 plaque size, or host range restriction.

1 39. The isolated polynucleotide molecule of claim
2 33, wherein said chimeric genome or antigenome incorporates at
3 least one and up to a full complement of mutations present in
4 rcp45, rcp45 3'NCMFHN, rcp45 3'NL, rcp45 3'N, or rcp45 F.

1 40. The isolated polynucleotide molecule of claim
2 33, wherein a mutation specifying a phenotypic alteration
3 selected from attenuation, temperature-sensitivity, cold-
4 adaptation, small plaque size, host range restriction, or a
5 change in an immunogenic epitope of PIV is incorporated in a
6 chimeric PIV background comprising a genome or antigenome
7 having one or more PIV3 HN or F glycoprotein genes substituted
8 by one or more counterpart PIV1 or PIV2 HN and F glycoprotein
9 genes.

1 41. The isolated polynucleotide molecule of claim
2 33, wherein the heterologous sequence specifies a phenotypic
3 alteration selected from attenuation, temperature-sensitivity,

4 cold-adaptation, small plaque size, host range restriction, or
5 a change in an immunogenic epitope of a chimeric PIV.

1 42. The isolated polynucleotide molecule of claim
2 11, which incorporates a cis-acting regulatory sequence of
3 HPIV1, HPIV2, BPIV or MPIV.

1 43. The isolated polynucleotide molecule of claim
2 11, which incorporates a heterologous sequence from RSV.

1 44. The isolated polynucleotide molecule of claim
2 43, wherein the heterologous sequence from RSV is a G or F
3 gene or gene segment.

1 45. The isolated polynucleotide molecule of claim
2 11, which incorporates a heterologous sequence from measles
3 virus.

1 46. The isolated polynucleotide molecule of claim
2 45, wherein the heterologous sequence from measles virus is a
3 HA or F gene or gene segment.

1 47. The isolated polynucleotide molecule of claim
2 11, which incorporates a polynucleotide sequence encoding a
3 non-PIV molecule selected from a cytokine, a T-helper epitope,
4 a restriction site marker, or a protein of a microbial
5 pathogen capable of eliciting a protective immune response in
6 a mammalian host.

1 48. A cell or cell-free composition including an
2 expression vector which comprises an isolated polynucleotide
3 molecule encoding a PIV genome or antigenome and an expression
4 vector which comprises one or more isolated polynucleotide
5 molecules that encode(s) N, P and L proteins of PIV, whereby
6 expression of said PIV genome or antigenome and N, P, and L
7 proteins yields an infectious PIV particle.

1 49. The cell or cell-free composition of claim 48,
2 wherein the infectious PIV particle is a virus.

1 50. The cell or cell-free composition of claim 48,
2 wherein the infectious PIV particle is a subviral particle.

1 51. The cell or cell-free composition of claim 48,
2 wherein the polynucleotide encoding the PIV genome or
3 antigenome and the one or more polynucleotides encoding N, P
4 and L proteins of PIV are incorporated within a single vector.

1 52. A method for producing an infectious PIV
2 particle from one or more isolated polynucleotide molecules
3 encoding said PIV, comprising:
4 coexpressing in a cell or cell-free system an
5 expression vector which comprises a polynucleotide molecule
6 encoding a PIV genome or antigenome and an expression vector
7 which comprises one or more polynucleotide molecules encoding
8 N, P and L proteins, thereby producing an infectious PIV
9 particle.

1 53. The method of claim 52, wherein the PIV genome
2 or antigenome and the N, P, and L proteins are expressed by
3 the same expression vector.

1 54. The method of claim 52, wherein the N, P, and L
2 proteins are encoded on two or three different expression
3 vectors.

1 55. The method of claim 52, wherein at least one of
2 the N, P and L proteins is supplied by coinfection with PIV.

1 56. The method of claim 52, wherein the
2 polynucleotide molecule that encodes the PIV genome or
3 antigenome is cDNA.

1 57. The method of claim 52, wherein the infectious
2 PIV particle is a virus.

1 58. The method of claim 52, wherein the infectious
2 PIV particle is a subviral particle.

1 59. The method of claim 52, wherein the
2 polynucleotide molecule encoding the PIV genome or antigenome
3 is a human, bovine or murine PIV sequence.

1 60. The method of claim 52, wherein the
2 polynucleotide molecule encoding the PIV genome or antigenome
3 encodes the sequence of a wild-type PIV strain.

1 61. The method of claim 52, wherein the
2 polynucleotide molecule encoding the PIV genome or antigenome
3 encodes HPIV3.

1 62. The method of claim 52, wherein the
2 polynucleotide molecule encoding the PIV genome or antigenome
3 incorporates an attenuating mutation from a biologically
4 derived PIV strain.

1 63. The method of claim 52, wherein the
2 polynucleotide molecule encoding the PIV genome or antigenome
3 incorporates one or more *ts* mutations.

1 64. The method of claim 52, wherein the
2 polynucleotide molecule encoding the PIV genome or antigenome
3 incorporates one or more non-*ts* attenuating mutations.

1 65. The method of claim 52, wherein the
2 polynucleotide molecule encoding the PIV genome or antigenome
3 incorporates at least one mutation of JS *cp45*.

1 66. The method of claim 65, wherein the
2 polynucleotide molecule encoding the PIV genome or antigenome
3 incorporates multiple mutations of JS *cp45*.

1 67. The method of claim 65, wherein the mutation of
2 JS *cp45* specifies at least one amino acid substitution in the
3 polymerase L protein.

1 68. The method of claim 67, wherein the amino acid
2 substitution in the polymerase L occurs at a position
3 corresponding to Tyr₉₄₂, Leu₉₉₂, or Thr₁₅₅₈ of JS *cp45*.

1 69. The method of claim 65, wherein said mutation
2 of JS *cp45* specifies a change in a PIV protein selected from
3 L, M, N, C, F, or HN or in a PIV extragenic sequence selected
4 from a 3' leader or N gene start sequence.

1 70. The method of claim 52, wherein said
2 polynucleotide molecule encoding the PIV genome or antigenome
3 incorporates a mutation that is stabilized by multiple
4 nucleotide substitutions in a codon which specifies the
5 mutation.

1 71. The method of claim 52, wherein said
2 polynucleotide molecule encoding said PIV genome or antigenome
3 incorporates a plurality and up to a full complement of
4 mutations present in *rcp45*, *rcp45* 3'NCMFHN, *rcp45* 3'NL, *rcp45*
5 3'N, or *rcp45* F.

1 72. The method of claim 69, wherein said
2 polynucleotide molecule encoding said PIV genome or antigenome
3 is an antigenomic cDNA selected from *rcp45*, *rcp45* 3'NCMFHN,
4 *rcp45* 3'NL, *rcp45* 3'N, *rcp45* L, *rcp45* F, *rcp45* M, *rcp45* HN, or
5 *rcp45* C.

1 73. The method of claim 52, wherein said
2 polynucleotide molecule encoding said PIV genome or antigenome
3 incorporates a heterologous sequence from HPIV1, HPIV2, HPIV3,
4 BPIV or MPIV to form a chimeric genome or antigenome.

1 74. The method of claim 73, wherein the
2 polynucleotide molecule encoding the PIV genome or antigenome

3 is a chimera of a HPIV3 sequence and a HPIV1, HPIV2, BPIV or
4 MPIV sequence.

1 75. The method of claim 74, wherein a heterologous
2 sequence from HPIV1 or HPIV2 encoding a gene or gene segment
3 of an HN or F glycoprotein is substituted for a corresponding
4 gene or gene segment of HPIV3.

1 76. The method of claim 73, wherein said chimeric
2 genome or antigenome incorporates one or more *ts* mutations.

1 77. The method of claim 73, wherein said chimeric
2 genome or antigenome incorporates one or more non-*ts*
3 attenuating mutations.

1 78. The method of claim 73, wherein said chimeric
2 genome or antigenome incorporates one or more mutations of JS
3 cp45.

1 79. The method of claim 73, wherein said chimeric
2 genome or antigenome incorporates multiple mutations each
3 specifying a phenotype selected from attenuation, temperature-
4 sensitivity, cold-adaptation, small plaque size, or host range
5 restriction.

1 80. The method of claim 73, wherein a mutation
2 specifying a phenotypic alteration selected from attenuation,
3 temperature-sensitivity, cold-adaptation, small plaque size,
4 host range restriction, or a change in an immunogenic epitope
5 of PIV is incorporated in a chimeric PIV background comprising
6 a genome or antigenome having one or more PIV3 HN or F
7 glycoprotein genes substituted by one or more counterpart PIV1
8 or PIV2 HN and F glycoprotein genes.

1 81. The method of claim 80, wherein one or more
2 mutations of JS cp45 are incorporated in a chimeric background
3 comprising a genome or antigenome having both PIV3 HN and F

4 glycoprotein genes substituted by counterpart PIV1 or PIV2 HN
5 and F glycoprotein genes.

1 82. The method of claim 81, wherein said one or
2 more mutations of JS *cp45* occur in one or more PIV proteins
3 selected from L, M, N, C, F, or HN or in a PIV extragenic
4 sequence selected from a 3' leader or N gene start sequence.

1 83. The method of claim 73, wherein the
2 heterologous sequence specifies a phenotypic alteration
3 selected from attenuation, temperature-sensitivity, cold-
4 adaptation, small plaque size, host range restriction, or a
5 change in an immunogenic epitope of a chimeric PIV.

1 84. The method of claim 52, wherein said
2 polynucleotide molecule encoding said PIV genome or antigenome
3 incorporates a heterologous sequence from RSV.

1 85. The method of claim 84, wherein the
2 heterologous sequence from RSV is a G or F gene or gene
3 segment.

1 86. The method of claim 52, wherein said
2 polynucleotide molecule encoding said PIV genome or antigenome
3 incorporates a heterologous sequence from measles virus.

1 87. The method of claim 86, wherein the
2 heterologous sequence from measles virus is a HA or F gene or
3 gene segment.

1 88. The method of claim 52, wherein the
2 polynucleotide molecule encoding the PIV genome or antigenome
3 is selected from:

4 i) p218(131) (SEQ ID NO: 1);
5 ii) p3/7(131) (SEQ ID NO: 14);
6 iii) p3/7(131)2G (SEQ ID NO: 15); or
7 iv) the polynucleotide molecule of i), ii) or iii)
8 modified by introduction of a heterologous PIV sequence

9 selected from a HPIV1 sequence, a HPIV2 sequence, a BPIV
10 sequence or a MPIV sequence or by a nucleotide insertion,
11 rearrangement, deletion or substitution specifying a
12 phenotypic alteration selected from attenuation, temperature-
13 sensitivity, cold-adaptation, small plaque size, host range
14 restriction, or a change in an immunogenic epitope of PIV.

1 89. The method of claim 52, wherein the
2 polynucleotide molecule encoding the PIV genome or antigenome
3 is selected from:
4 i) p218(131) (SEQ ID NO: 1);
5 ii) p3/7(131) (SEQ ID NO: 14);
6 iii) p3/7(131)2G (SEQ ID NO: 15); or
7 iv) the polynucleotide molecule of i), ii) or iii)
8 modified by introduction of a heterologous PIV sequence
9 selected from a HPIV1 sequence, a HPIV2 sequence, a BPIV
10 sequence or a MPIV sequence and by a nucleotide insertion,
11 rearrangement, deletion or substitution different from said
12 introduction of said heterologous PIV sequence specifying a
13 phenotypic alteration selected from attenuation, temperature-
14 sensitivity, cold-adaptation, small plaque size, host range
15 restriction, or a change in an immunogenic epitope of PIV.

1 90. The method of claim 52, wherein the
2 polynucleotide molecule encoding the PIV genome or antigenome
3 is modified to encode a non-PIV molecule selected from a
4 cytokine, a T-helper epitope, a restriction site marker, or a
5 protein of a microbial pathogen capable of eliciting a
6 protective immune response in a mammalian host.

1 91. An isolated infectious PIV particle which
2 comprises a recombinant PIV genome or antigenome, a N protein,
3 a P protein, and a L protein.

1 92. The isolated infectious PIV particle of claim
2 91, which is a subviral particle.

1 93. The isolated infectious PIV particle of claim
2 91, which is a virus.

1 94. The isolated infectious PIV particle of claim
2 91, wherein the recombinant PIV genome or antigenome
3 incorporates a heterologous sequence from RSV or measles
4 virus.

1 95. The isolated infectious PIV particle of claim
2 91, wherein the recombinant PIV genome or antigenome is a
3 cDNA.

1 96. The isolated infectious PIV particle of claim
2 91, which is a human PIV.

1 97. The isolated infectious PIV particle of claim
2 91, wherein the recombinant PIV genome or antigenome is a
3 chimera of heterologous PIV sequences selected from HPIV1,
4 HPIV2, HPIV3, BPIV, or MPIV sequences.

1 98. The isolated infectious PIV particle of claim
2 91, wherein the recombinant PIV genome or antigenome is
3 selected from:
4 i) p218(131) (SEQ ID NO: 1);
5 ii) p3/7(131) (SEQ ID NO: 14);
6 iii) p3/7(131)2G (SEQ ID NO: 15); or
7 iv) the genome or antigenome of i), ii) or iii)
8 modified by introduction of a heterologous PIV sequence
9 selected from a HPIV1 sequence, a HPIV2 sequence, a BPIV
10 sequence or a MPIV sequence or by a nucleotide insertion,
11 rearrangement, deletion or substitution specifying a
12 phenotypic alteration selected from attenuation, temperature-
13 sensitivity, cold-adaptation, small plaque size, host range
14 restriction, or a change in an immunogenic epitope of PIV.

1 99. The isolated infectious PIV particle of claim
2 91, wherein the recombinant PIV genome or antigenome is
3 selected from:

4 i) p218(131) (SEQ ID NO: 1);
5 ii) p3/7(131) (SEQ ID NO: 14);
6 iii) p3/7(131)2G (SEQ ID NO: 15); or
7 iv) the genome or antigenome of i), ii) or iii)
8 modified by introduction of a heterologous PIV sequence
9 selected from a HPIV1 sequence, a HPIV2 sequence, a BPIV
10 sequence or a MPIV sequence and by a nucleotide insertion,
11 rearrangement, deletion or substitution different from said
12 introduction of said heterologous PIV sequence specifying a
13 phenotypic alteration selected from attenuation, temperature-
14 sensitivity, cold-adaptation, small plaque size, host range
15 restriction, or a change in an immunogenic epitope of PIV.

1 100. The isolated infectious PIV particle of claim
2 91, wherein the counterpart gene or gene segment is a gene or
3 gene segment of the HN or F glycoprotein gene of HPIV1 or
4 HPIV2.

1 101. The isolated infectious PIV particle of claim
2 91, wherein the recombinant PIV genome or antigenome
3 incorporates a heterologous sequence from RSV or measles
4 virus.

1 102. The isolated infectious PIV particle of claim
2 91, wherein the recombinant PIV genome or antigenome is
3 modified by a nucleotide insertion, rearrangement, deletion or
4 substitution encoding a phenotypic alteration selected from
5 attenuation, temperature-sensitivity, cold-adaptation, small
6 plaque size, host range restriction, or a change in an
7 immunogenic epitope of PIV.

1 103. The isolated infectious PIV particle of claim
2 91, wherein the recombinant PIV genome or antigenome
3 incorporates multiple *ts* mutations.

1 104. The isolated infectious PIV particle of claim
2 91, wherein the recombinant PIV genome or antigenome
3 incorporates multiple non-*ts* attenuating mutations.

1 105. The isolated infectious PIV particle of claim
2 91, wherein the recombinant PIV genome or antigenome
3 incorporates at least one mutation of JS *cp45*.

1 106. The isolated infectious PIV particle of claim
2 105, wherein the mutation of JS *cp45* specifies an amino acid
3 substitution in the polymerase L protein.

1 107. The isolated infectious PIV particle of claim
2 97, wherein said chimeric genome or antigenome incorporates
3 one or more *ts* mutations.

1 108. The isolated infectious PIV particle of claim
2 97, wherein said chimeric genome or antigenome incorporates
3 one or more non-*ts* attenuating mutations.

1 109. The isolated infectious PIV particle of claim
2 97, wherein said chimeric genome or antigenome incorporates
3 one or more mutations of JS *cp45*.

1 110. The isolated infectious PIV particle of claim
2 129, wherein said chimeric genome or antigenome incorporates
3 multiple mutations each specifying a phenotype selected from
4 attenuation, temperature-sensitivity, cold-adaptation, small
5 plaque size, or host range restriction.

1 111. The isolated infectious PIV particle of claim
2 109, wherein said chimeric genome or antigenome incorporates
3 at least one and up to a full complement of mutations present
4 in *rcp45*, *rcp45* 3'NCMFHN, *rcp45* 3'NL, *rcp45* 3'N, or *rcp45* F.

1 112. The isolated infectious PIV particle of claim
2 91, wherein a mutation specifying a phenotypic alteration
3 selected from attenuation, temperature-sensitivity, cold-
4 adaptation, small plaque size, host range restriction, or a
5 change in an immunogenic epitope of PIV is incorporated in a
6 chimeric PIV background comprising a genome or antigenome
7 having one or more PIV3 HN or F glycoprotein genes or gene

8 segments substituted by one or more counterpart PIV1 or PIV2
9 HN and F glycoprotein genes or gene segments.

1 113. The isolated infectious PIV particle of claim
2 112, wherein one or more mutations of JS cp45 are incorporated
3 in said chimeric background.

1 114. The isolated infectious PIV particle of claim
2 of claim 113, wherein said one or more mutations of JS cp45
3 occur in one or more PIV proteins selected from L, M, N, C, F,
4 or HN or in a PIV extragenic sequence selected from a 3'
5 leader or N gene start sequence.

1 115. The isolated infectious PIV particle of claim
2 91, wherein the recombinant PIV genome or antigenome is
3 modified to encode a non-PIV molecule selected from a
4 cytokine, a T-helper epitope, a restriction site marker, or a
5 protein of a microbial pathogen capable of eliciting a
6 protective immune response in a mammalian host.

1 116. The isolated infectious PIV particle of claim
2 91, further comprising an RSV antigen or epitope which elicits
3 protective immunity to RSV in an immunized host.

1 117. The isolated infectious PIV particle of claim
2 91, which is selected from r942, r992, r1558, r942/992,
3 r992/1558, r942/1558, or r942/992/1558, rcp45 3'N, rcp45 C,
4 rcp45 M, rcp45 F, rcp45 HN, rcp45L, rcp45 3'NL, rcp45
5 3'NCMFHN, and rcp45.

1 118. An immunogenic composition comprising an
2 immunogenically effective amount of an infectious PIV particle
3 in a pharmaceutically acceptable carrier, said PIV particle
4 comprising a recombinant PIV genome or antigenome, a N
5 protein, a P protein, and a L protein.

1 119. The immunogenic composition of claim 118,
2 wherein said infectious PIV particle is a subviral particle.

1 120. The immunogenic composition of claim 118,
2 wherein said infectious PIV particle is a virus.

1 121. The immunogenic composition of claim 118,
2 wherein the recombinant PIV genome or antigenome incorporates
3 a heterologous sequence from RSV or measles virus.

1 122. The immunogenic composition of claim 118,
2 wherein the recombinant PIV genome or antigenome is a chimera
3 of heterologous PIV sequences selected from HPIV1, HPIV2,
4 HPIV3, BPIV, or MPIV sequences to form an infectious, chimeric
5 PIV particle.

1 123. The immunogenic composition of claim 118,
2 wherein the recombinant PIV genome or antigenome encodes a
3 human PIV in which a gene or gene segment is replaced with a
4 counterpart gene or gene segment from a heterologous PIV.

1 124. The immunogenic composition of claim 123,
2 wherein one or both HN and F glycoprotein genes of HPIV1 are
3 substituted for HN and F glycoprotein genes of HPIV3 to form
4 said infectious, chimeric PIV particle.

1 125. The immunogenic composition of claim 123,
2 wherein the recombinant PIV genome or antigenome of said
3 infectious, chimeric PIV particle is modified by a nucleotide
4 insertion, rearrangement, deletion or substitution encoding a
5 phenotypic alteration selected from attenuation, temperature-
6 sensitivity, cold-adaptation, small plaque size, host range
7 restriction, or a change in an immunogenic epitope of PIV.

1 126. The immunogenic composition of claim 125,
2 wherein said recombinant PIV genome or antigenome incorporates
3 multiple mutations selected from *ts* and non-*ts* attenuating
4 mutations to form an attenuated, infectious, chimeric PIV
5 particle.

1 127. The immunogenic composition of claim 118,
2 wherein the recombinant PIV genome or antigenome incorporates
3 a mutation of JS *cp45*.

1 128. The immunogenic composition of claim 118,
2 wherein the recombinant PIV genome or antigenome incorporates
3 multiple mutations of JS *cp45*.